

Iñaki Comas

List of Publications by Year in descending order

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Version: 2024-02-01

130
papers

9,271
citations

81900

39
h-index

49909

87
g-index

151
all docs

151
docs citations

151
times ranked

9772
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Recurrences of multidrug-resistant tuberculosis: Strains involved, within-host diversity, and fine-tuned allocation of reinfections. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 327-336. | 3.0 | 6 |
| 2 | Immunological response against SARS-CoV-2 following full-dose administration of Comirnaty® COVID-19 vaccine in nursing home residents. <i>Clinical Microbiology and Infection</i> , 2022, 28, 279-284. | 6.0 | 17 |
| 3 | Systematic Genomic and Clinical Analysis of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfections and Recurrences Involving the Same Strain. <i>Emerging Infectious Diseases</i> , 2022, 28, 86-95. | 4.3 | 8 |
| 4 | Severe Acute Respiratory Syndrome Coronavirus 2 Adaptive Immunity in Nursing Home Residents Following a Third Dose of the Comirnaty Coronavirus Disease 2019 Vaccine. <i>Clinical Infectious Diseases</i> , 2022, 75, e865-e868. | 5.8 | 12 |
| 5 | SARS-CoV-2 adaptive immunity in nursing home residents up to eight months after two doses of the Comirnaty® COVID-19 vaccine. <i>Journal of Infection</i> , 2022, 84, 834-872. | 3.3 | 2 |
| 6 | SNPs in Genes Related to DNA Damage Repair in Mycobacterium Tuberculosis: Their Association with Type 2 Diabetes Mellitus and Drug Resistance. <i>Genes</i> , 2022, 13, 609. | 2.4 | 3 |
| 7 | The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273. | 7.3 | 114 |
| 8 | SARS-CoV-2 Delta variant breakthrough infections in nursing home residents at midterm after Comirnaty® COVID-19 vaccination. <i>Journal of Medical Virology</i> , 2022, 94, 3776-3782. | 5.0 | 6 |
| 9 | Gene evolutionary trajectories in <i>Mycobacterium tuberculosis</i> reveal temporal signs of selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113600119. | 7.1 | 13 |
| 10 | SARS-CoV-2 Omicron BA.1 variant breakthrough infections in nursing home residents after an homologous third dose of the Comirnaty® COVID-19 vaccine: Looking for correlates of protection. <i>Journal of Medical Virology</i> , 2022, 94, 4216-4223. | 5.0 | 15 |
| 11 | Whole genome sequencing analysis to evaluate the influence of T2DM on polymorphisms associated with drug resistance in <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2022, 23, . | 2.8 | 1 |
| 12 | Fine-grain population structure and transmission patterns of Mycobacterium tuberculosis in southern Mozambique, a high TB/HIV burden area. <i>Microbial Genomics</i> , 2022, 8, . | 2.0 | 4 |
| 13 | The structural role of SARS-CoV-2 genetic background in the emergence and success of spike mutations: The case of the spike A222V mutation. <i>PLoS Pathogens</i> , 2022, 18, e1010631. | 4.7 | 11 |
| 14 | B-type natriuretic peptide over N-terminal pro-brain natriuretic peptide to predict incident atrial fibrillation after cryptogenic stroke. <i>European Journal of Neurology</i> , 2021, 28, 540-547. | 3.3 | 20 |
| 15 | Whole genomic sequencing based genotyping reveals a specific X3 sublineage restricted to Mexico and related with multidrug resistance. <i>Scientific Reports</i> , 2021, 11, 1870. | 3.3 | 8 |
| 16 | Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60. | 1.6 | 13 |
| 17 | Epidemiological, clinical and genomic snapshot of the first 100 B.1.1.7 SARS-CoV-2 cases in Madrid. <i>Journal of Travel Medicine</i> , 2021, 28, . | 3.0 | 3 |
| 18 | Whole-genome sequencing for TB source investigations: principles of ethical precision public health. <i>International Journal of Tuberculosis and Lung Disease</i> , 2021, 25, 222-227. | 1.2 | 1 |

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|----|--|------|-----------|
| 19 | Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60. | 1.6 | 21 |
| 20 | Overlapping prison/community tuberculosis outbreaks in Costa Rica revealed by alternative analysis of suboptimal material. <i>Transboundary and Emerging Diseases</i> , 2021, , . | 3.0 | 0 |
| 21 | Integrative transnational analysis to dissect tuberculosis transmission events along the migratory route from Africa to Europe. <i>Journal of Travel Medicine</i> , 2021, 28, . | 3.0 | 7 |
| 22 | Genomic analyses of Mycobacterium tuberculosis from human lung resections reveal a high frequency of polyclonal infections. <i>Nature Communications</i> , 2021, 12, 2716. | 12.8 | 25 |
| 23 | Proper Assignment of Reactivation in a COVID-19 Recurrence Initially Interpreted as a Reinfection. <i>Journal of Infectious Diseases</i> , 2021, 224, 788-792. | 4.0 | 5 |
| 24 | SplitStrains, a tool to identify and separate mixed Mycobacterium tuberculosis infections from WGS data. <i>Microbial Genomics</i> , 2021, 7, . | 2.0 | 7 |
| 25 | Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712. | 27.8 | 363 |
| 26 | Heterogeneous Streptomycin Resistance Level Among Mycobacterium tuberculosis Strains From the Same Transmission Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 659545. | 3.5 | 10 |
| 27 | Different Within-Host Viral Evolution Dynamics in Severely Immunosuppressed Cases with Persistent SARS-CoV-2. <i>Biomedicines</i> , 2021, 9, 808. | 3.2 | 28 |
| 28 | Overlapping of Independent SARS-CoV-2 Nosocomial Transmissions in a Complex Outbreak. <i>MSphere</i> , 2021, 6, e0038921. | 2.9 | 9 |
| 29 | Host Genetic Analysis Should Be Mandatory for Proper Classification of COVID-19 Reinfections. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab402. | 0.9 | 1 |
| 30 | The Sputum Microbiome in Pulmonary Tuberculosis and Its Association With Disease Manifestations: A Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2021, 12, 633396. | 3.5 | 9 |
| 31 | The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. <i>Nature Genetics</i> , 2021, 53, 1405-1414. | 21.4 | 35 |
| 32 | Complete Analysis of the Epidemiological Scenario around a SARS-CoV-2 Reinfection: Previous Infection Events and Subsequent Transmission. <i>MSphere</i> , 2021, 6, e0059621. | 2.9 | 4 |
| 33 | Expanded tracking of a Beijing Mycobacterium tuberculosis strain involved in an outbreak in France. <i>Travel Medicine and Infectious Disease</i> , 2021, 44, 102167. | 3.0 | 2 |
| 34 | An evolutionary functional genomics approach identifies novel candidate regions involved in isoniazid resistance in Mycobacterium tuberculosis. <i>Communications Biology</i> , 2021, 4, 1322. | 4.4 | 5 |
| 35 | Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. <i>MBio</i> , 2021, 12, e0231521. | 4.1 | 6 |
| 36 | A Genomic Snapshot of the SARS-CoV-2 Pandemic in the Balearic Islands. <i>Frontiers in Microbiology</i> , 2021, 12, 803827. | 3.5 | 3 |

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|----|---|------|-----------|
| 37 | SARS-CoV-2 Outbreak on a Spanish Mink Farm: Epidemiological, Molecular, and Pathological Studies. <i>Frontiers in Veterinary Science</i> , 2021, 8, 805004. | 2.2 | 14 |
| 38 | Accuracy of an amplicon-sequencing nanopore approach to identify variants in tuberculosis drug-resistance-associated genes. <i>Microbial Genomics</i> , 2021, 7, . | 2.0 | 7 |
| 39 | Towards next-generation diagnostics for tuberculosis: identification of novel molecular targets by large-scale comparative genomics. <i>Bioinformatics</i> , 2020, 36, 985-989. | 4.1 | 13 |
| 40 | Characterization of Polymorphisms Associated with Multidrug-Resistant Tuberculosis by Whole Genomic Sequencing: A Preliminary Report from Mexico. <i>Microbial Drug Resistance</i> , 2020, 26, 732-740. | 2.0 | 4 |
| 41 | Uso de las tecnologías de secuenciación masiva para el diagnóstico y epidemiología de enfermedades infecciosas. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2020, 38, 32-38. | 0.5 | 1 |
| 42 | Whole-genome sequencing of <i>Mycobacterium tuberculosis</i> directly from clinical samples for high-resolution genomic epidemiology and drug resistance surveillance: an observational study. <i>Lancet Microbe</i> , The, 2020, 1, e175-e183. | 7.3 | 42 |
| 43 | Glucocorticoid-dependent transcription in skin requires epidermal expression of the glucocorticoid receptor and is modulated by the mineralocorticoid receptor. <i>Scientific Reports</i> , 2020, 10, 18954. | 3.3 | 4 |
| 44 | <i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901. | 10.3 | 33 |
| 45 | GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460. | 8.9 | 25 |
| 46 | Contaminant DNA in bacterial sequencing experiments is a major source of false genetic variability. <i>BMC Biology</i> , 2020, 18, 24. | 3.8 | 53 |
| 47 | Specificity and mutagenesis bias of the mycobacterial alternative mismatch repair analyzed by mutation accumulation studies. <i>Science Advances</i> , 2020, 6, eaay4453. | 10.3 | 30 |
| 48 | Screening of inmates transferred to Spain reveals a Peruvian prison as a reservoir of persistent <i>Mycobacterium tuberculosis</i> MDR strains and mixed infections. <i>Scientific Reports</i> , 2020, 10, 2704. | 3.3 | 12 |
| 49 | <i>Mycobacterium tuberculosis</i> associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1 β production. <i>Nature Communications</i> , 2020, 11, 1949. | 12.8 | 52 |
| 50 | Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, . | 7.0 | 186 |
| 51 | Tuberculosis in Liberia: high multidrug-resistance burden, transmission and diversity modelled by multiple importation events. <i>Microbial Genomics</i> , 2020, 6, . | 2.0 | 11 |
| 52 | The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. <i>Archivos De Bronconeumología</i> , 2019, 55, 421-426. | 0.8 | 0 |
| 53 | The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. <i>Archivos De Bronconeumología</i> , 2019, 55, 421-426. | 0.8 | 7 |
| 54 | Development and application of affordable SNP typing approaches to genotype <i>Mycobacterium tuberculosis</i> complex strains in low and high burden countries. <i>Scientific Reports</i> , 2019, 9, 15343. | 3.3 | 8 |

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|----|---|------|-----------|
| 55 | High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. <i>PLoS Medicine</i> , 2019, 16, e1002961. | 8.4 | 62 |
| 56 | Influence of Gut Microbiota on Progression to Tuberculosis Generated by High Fat Diet-Induced Obesity in C3HeB/FeJ Mice. <i>Frontiers in Immunology</i> , 2019, 10, 2464. | 4.8 | 26 |
| 57 | Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994. | 12.8 | 33 |
| 58 | Evolutionary Dissection of the Dot/Icm System Based on Comparative Genomics of 58 <i>Legionella</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 2619-2632. | 2.5 | 12 |
| 59 | Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545. | 28.6 | 237 |
| 60 | Whole genomic sequencing as a tool for diagnosis of drug and multidrug-resistance tuberculosis in an endemic region in Mexico. <i>PLoS ONE</i> , 2019, 14, e0213046. | 2.5 | 20 |
| 61 | Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307. | 10.3 | 61 |
| 62 | DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249. | 4.1 | 38 |
| 63 | Cryptic Resistance Mutations Associated With Misdiagnoses of Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2019, 220, 316-320. | 4.0 | 19 |
| 64 | Simplified Model to Survey Tuberculosis Transmission in Countries Without Systematic Molecular Epidemiology Programs. <i>Emerging Infectious Diseases</i> , 2019, 25, 507-514. | 4.3 | 5 |
| 65 | Large genomics datasets shed light on the evolution of the <i>Mycobacterium tuberculosis</i> complex. <i>Infection, Genetics and Evolution</i> , 2019, 72, 10-15. | 2.3 | 11 |
| 66 | Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282. | 4.1 | 71 |
| 67 | Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191. | 1.8 | 103 |
| 68 | Whole genome sequencing-based analysis of tuberculosis (TB) in migrants: rapid tools for cross-border surveillance and to distinguish between recent transmission in the host country and new importations. <i>Eurosurveillance</i> , 2019, 24, . | 7.0 | 22 |
| 69 | Tuberculosis of the elbow: A rare form of presentation of extrapulmonary tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2019, 37, 550-551. | 0.5 | 1 |
| 70 | Gene expression models based on a reference laboratory strain are poor predictors of <i>Mycobacterium tuberculosis</i> complex transcriptional diversity. <i>Scientific Reports</i> , 2018, 8, 3813. | 3.3 | 14 |
| 71 | Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415. | 27.0 | 405 |
| 72 | China's tuberculosis epidemic stems from historical expansion of four strains of <i>Mycobacterium tuberculosis</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1982-1992. | 7.8 | 83 |

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|----|---|------|-----------|
| 73 | Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382. | 3.3 | 75 |
| 74 | TB Transmission: Closing the Gaps. <i>EBioMedicine</i> , 2018, 34, 4-5. | 6.1 | 1 |
| 75 | The Troika Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2018, 8, 1948. | 4.8 | 24 |
| 76 | Mycobacterium tuberculosis Acquires Limited Genetic Diversity in Prolonged Infections, Reactivations and Transmissions Involving Multiple Hosts. <i>Frontiers in Microbiology</i> , 2018, 8, 2661. | 3.5 | 12 |
| 77 | Whole-genome sequence analysis of the Mycobacterium avium complex and proposal of the transfer of Mycobacterium yongonense to Mycobacterium intracellulare subsp. yongonense subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1998-2005. | 1.7 | 25 |
| 78 | The effect size of type 2 diabetes mellitus on tuberculosis drug resistance and adverse treatment outcomes. <i>Tuberculosis</i> , 2017, 103, 83-91. | 1.9 | 33 |
| 79 | The Evolution of Antibiotic Resistance. , 2017, , 257-284. | | 3 |
| 80 | Genomic Epidemiology of Tuberculosis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 79-93. | 1.6 | 21 |
| 81 | A novel strategy based on genomics and specific PCR reveals how a multidrug-resistant Mycobacterium tuberculosis strain became prevalent in Equatorial Guinea 15 years after its emergence. <i>Clinical Microbiology and Infection</i> , 2017, 23, 92-97. | 6.0 | 11 |
| 82 | A standardised method for interpreting the association between mutations and phenotypic drug resistance in Mycobacterium tuberculosis. <i>European Respiratory Journal</i> , 2017, 50, 1701354. | 6.7 | 273 |
| 83 | In-Depth Characterization and Functional Analysis of Clonal Variants in a Mycobacterium tuberculosis Strain Prone to Microevolution. <i>Frontiers in Microbiology</i> , 2017, 8, 694. | 3.5 | 11 |
| 84 | Draft Genome Sequence of Mycobacterium brumae ATCC 51384. <i>Genome Announcements</i> , 2016, 4, . | 0.8 | 4 |
| 85 | New Genome-Wide Algorithm Identifies Novel In-Vivo Expressed Mycobacterium Tuberculosis Antigens Inducing Human T-Cell Responses with Classical and Unconventional Cytokine Profiles. <i>Scientific Reports</i> , 2016, 6, 37793. | 3.3 | 69 |
| 86 | Subtle genotypic changes can be observed soon after diagnosis in Mycobacterium tuberculosis infection. <i>International Journal of Medical Microbiology</i> , 2016, 306, 401-405. | 3.6 | 5 |
| 87 | Genomic Analysis of Bacterial Outbreaks. , 2016, , 203-232. | | 0 |
| 88 | Urgent Implementation in a Hospital Setting of a Strategy To Rule Out Secondary Cases Caused by Imported Extensively Drug-Resistant Mycobacterium tuberculosis Strains at Diagnosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2969-2974. | 3.9 | 15 |
| 89 | Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543. | 21.4 | 326 |
| 90 | Legionella effectors reflect strength in diversity. <i>Nature Genetics</i> , 2016, 48, 115-116. | 21.4 | 1 |

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|-----|---|------|-----------|
| 91 | Ultrafast Assessment of the Presence of a High-Risk Mycobacterium tuberculosis Strain in a Population. <i>Journal of Clinical Microbiology</i> , 2016, 54, 779-781. | 3.9 | 18 |
| 92 | Phylogenetic analysis of vitamin B12-related metabolism in Mycobacterium tuberculosis. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 6. | 3.5 | 27 |
| 93 | Draft Genome Sequences of Mycobacterium setense Type Strain DSM-45070 and the Nonpathogenic Strain Manresensis, Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain. <i>Genome Announcements</i> , 2015, 3, . | 0.8 | 11 |
| 94 | Population Genomics of Mycobacterium tuberculosis in Ethiopia Contradicts the Virgin Soil Hypothesis for Human Tuberculosis in Sub-Saharan Africa. <i>Current Biology</i> , 2015, 25, 3260-3266. | 3.9 | 94 |
| 95 | Southern East Asian origin and coexpansion of Mycobacterium tuberculosis Beijing family with Han Chinese. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8136-8141. | 7.1 | 142 |
| 96 | Persistent Infection by a Mycobacterium tuberculosis Strain That Was Theorized To Have Advantageous Properties, as It Was Responsible for a Massive Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3423-3429. | 3.9 | 21 |
| 97 | Fast and low-cost decentralized surveillance of transmission of tuberculosis based on strain-specific PCRs tailored from whole genome sequencing data: a pilot study. <i>Clinical Microbiology and Infection</i> , 2015, 21, 249.e1-249.e9. | 6.0 | 22 |
| 98 | Comment on: Characterization of the embB gene in Mycobacterium tuberculosis isolates from Barcelona and rapid detection of main mutations related to ethambutol resistance using a low-density DNA array. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2298-2299. | 3.0 | 8 |
| 99 | Whole Genome Sequencing Analysis of Inpatient Microevolution in Mycobacterium tuberculosis: Potential Impact on the Inference of Tuberculosis Transmission. <i>Journal of Infectious Diseases</i> , 2014, 209, 98-108. | 4.0 | 120 |
| 100 | Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497. | 27.8 | 506 |
| 101 | Recombination drives genome evolution in outbreak-related Legionella pneumophila isolates. <i>Nature Genetics</i> , 2014, 46, 1205-1211. | 21.4 | 76 |
| 102 | Genetic diversity within Mycobacterium tuberculosis complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453. | 1.9 | 11 |
| 103 | Evaluation of Customised Lineage-Specific Sets of MIRU-VNTR Loci for Genotyping Mycobacterium tuberculosis Complex Isolates in Ghana. <i>PLoS ONE</i> , 2014, 9, e92675. | 2.5 | 19 |
| 104 | Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182. | 21.4 | 900 |
| 105 | Genome-wide Mapping of Transcriptional Start Sites Defines an Extensive Leaderless Transcriptome in Mycobacterium tuberculosis. <i>Cell Reports</i> , 2013, 5, 1121-1131. | 6.4 | 283 |
| 106 | Mycobacterial Lineages Causing Pulmonary and Extrapulmonary Tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013, 19, 460-463. | 4.3 | 215 |
| 107 | Novel Mycobacterium tuberculosis Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976. | 4.3 | 100 |
| 108 | Mapping of Genotype-Phenotype Diversity among Clinical Isolates of Mycobacterium tuberculosis by Sequence-Based Transcriptional Profiling. <i>Genome Biology and Evolution</i> , 2013, 5, 1849-1862. | 2.5 | 69 |

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|-----|---|------|-----------|
| 109 | Evidence for Diversifying Selection in a Set of Mycobacterium tuberculosis Genes in Response to Antibiotic- and Nonantibiotic-Related Pressure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1326-1336. | 8.9 | 43 |
| 110 | Vacunes i evolució: Per què és important entendre la diversitat genètica dels patògens?. <i>Mètode Revista De Difusió De La Investigació De La Universitat De València</i> , 2013, . | 0.0 | 0 |
| 111 | The Genome of Mycobacterium Africanum West African 2 Reveals a Lineage-Specific Locus and Genome Erosion Common to the M. tuberculosis Complex. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1552. | 3.0 | 69 |
| 112 | Two New Rapid SNP-Typing Methods for Classifying Mycobacterium tuberculosis Complex into the Main Phylogenetic Lineages. <i>PLoS ONE</i> , 2012, 7, e41253. | 2.5 | 120 |
| 113 | Long-Range Transcriptional Control of an Operon Necessary for Virulence-Critical ESX-1 Secretion in Mycobacterium tuberculosis. <i>Journal of Bacteriology</i> , 2012, 194, 2307-2320. | 2.2 | 36 |
| 114 | Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110. | 21.4 | 475 |
| 115 | The Evolution of Antibiotic Resistance. , 2011, , 305-337. | | 6 |
| 116 | A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011, 19, 492-500. | 7.7 | 71 |
| 117 | Human Macrophage Responses to Clinical Isolates from the Mycobacterium tuberculosis Complex Discriminate between Ancient and Modern Lineages. <i>PLoS Pathogens</i> , 2011, 7, e1001307. | 4.7 | 258 |
| 118 | Quantifying Nonvertical Inheritance in the Evolution of Legionella pneumophila. <i>Molecular Biology and Evolution</i> , 2011, 28, 985-1001. | 8.9 | 47 |
| 119 | Sequence-Based Analysis Uncovers an Abundance of Non-Coding RNA in the Total Transcriptome of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2011, 7, e1002342. | 4.7 | 210 |
| 120 | Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503. | 21.4 | 642 |
| 121 | Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. <i>PLoS Pathogens</i> , 2010, 6, e1000735. | 4.7 | 100 |
| 122 | The Past and Future of Tuberculosis Research. <i>PLoS Pathogens</i> , 2009, 5, e1000600. | 4.7 | 130 |
| 123 | Genotyping of Genetically Monomorphic Bacteria: DNA Sequencing in Mycobacterium tuberculosis Highlights the Limitations of Current Methodologies. <i>PLoS ONE</i> , 2009, 4, e7815. | 2.5 | 377 |
| 124 | Unraveling the evolutionary history of the phosphoryl-transfer chain of the phosphoenolpyruvate:phosphotransferase system through phylogenetic analyses and genome context. <i>BMC Evolutionary Biology</i> , 2008, 8, 147. | 3.2 | 23 |
| 125 | Evolution of Snake Venom Disintegrins by Positive Darwinian Selection. <i>Molecular Biology and Evolution</i> , 2008, 25, 2391-2407. | 8.9 | 131 |
| 126 | From Phylogenetics to Phylogenomics: The Evolutionary Relationships of Insect Endosymbiotic β -Proteobacteria as a Test Case. <i>Systematic Biology</i> , 2007, 56, 1-16. | 5.6 | 52 |

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|-----|--|-----|-----------|
| 127 | Phylogenetic signal and functional categories in Proteobacteria genomes. BMC Evolutionary Biology, 2007, 7, S7. | 3.2 | 12 |
| 128 | The Evolutionary Origin of Xanthomonadales Genomes and the Nature of the Horizontal Gene Transfer Process. Molecular Biology and Evolution, 2006, 23, 2049-2057. | 8.9 | 44 |
| 129 | Validating viral quasispecies with digital organisms: a re-examination of the critical mutation rate. BMC Evolutionary Biology, 2005, 5, 5. | 3.2 | 21 |
| 130 | Horizontal Gene Transfer in the Molecular Evolution of Mannose PTS Transporters. Molecular Biology and Evolution, 2005, 22, 1673-1685. | 8.9 | 50 |